GGTCAGAGAC ATCAAGAAAT AACGCCGGAA CATTAGTGCA GGCAGCTTCC ACAGCAATGG 4200

CATCCTGGTC ATCCAGCGGA TAGTTAATGA TCAGCCCACT GACGCGTTGC GCGAGAAGAT 4260

TGTGCACCGC CGCTTTACAG GCTTCGACGC CGCTTCGTTC TACCATCGAC ACCACCACGC 4320

TGGCACCCAG TTGATCGGCG CGAGATTTAA TCGCCGCGAC AATTTGCGAC GGCGCGTGCA 4380

GGGCCAGACT GGAGGTGGCA ACGCCAATCA GCAACGACTG TTTGCCCGCC AGTTGTTGTG 4440

CCACGCGGTT GGGAATGTAA TTCAGCTCCG CCATCGCCGC TTCCACTTTT TCCCGCGTTT 4500

TCGCAGAAAC GTGGCTGGCC TGGTTCACCA CGCGGGAAAC GGTCTGATAA GAGACACCGG 4560

CATACTCTGC GACATCGTAT AACGTTACTG GTTTCACATT CACCACCCTG AATTGACTCT 4620

CTTCCGGGCG CTATCATGCC ATACCGCGAA AGGTTTTGCG CCATTCGATG GTGTCCGGGA 4680

TCTCGACGCT CTCCCTTATG CGACTCCTGC ATTAGGAAGC AGCCCAGTAG TAGGTTGAGG 4740

CCGTTGAGCA CCGCCGCCGC AAGGAATGGT GCATGCAAGG AGATGGCGCC CAACAGTCCC 4800

CCGGCCACGG GGCCTGCCAC CATACCCACG CCGAAACAAG CGCTCATGAG CCCGAAGTGG 4860

CGAGCCCGAT CTTCCCCATC GGTGATGTCG GCGATATAGG CGCCAGCAAC CGCACCTGTG 4920

GCGCCGGTGA TGCCGGCCAC GATGCGTCCG GCGTAGAGGA TCGAGATCTC GATCCCGCGA 4980

AATTAATACG ACTCACTATA GGGGAATTGT GAGCGGATAA CAATTCCCCT CTAGAAATAA 5040

TTTTGTTTAA CTTTAAGAAG GAGATATACA TATGGGCCAT CATCATCATC ATCACGTGAT 5100

CGACATCATC GGGACCAGCC CCACATCCTG GGAACAGGCG GCGGCGGAGG CGGTCCAGCG 5160

GGCGCGGGAT AGCGTCGATG ACATCCGCGT CGCTCGGGTC ATTGAGCAGG ACATGGCCGT 5220

GGACAGCGCC GGCAAGATCA CCTACCGCAT CAAGCTCGAA GTGTCGTTCA AGATGAGGCC 5280

GGCGCAACCG AGGGGCTCGA AACCACCGAG CGGTTCGCCT GAAACGGCGG CCGGCGCCGG 5340

TACTGTCGCG ACTACCCCCG CGTCGTCGCC GGTGACGTTG GCGGAGACCG GTAGCACGCT 5400

GCTCTACCCG CTGTTCAACC TGTGGGGTCC GGCCTTTCAC GAGAGGTATC CGAACGTCAC 5460

GATCACCGCT CAGGGCACCG GTTCTGGTGC CGGGATCGCG CAGGCCGCCG CCGGGACGGT 5520

CAACATTGGG GCCTCCGACG CCTATCTGTC GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT 5580

Fig. 5D

GATGAACATC GCGCTAGCCA TCTCCGCTCA GCAGGTCAAC TACAACCTGC CCGGAGTGAG 5640

CGAGCACCTC AAGCTGAACG GAAAAGTCCT GGCGGCCATG TACCAGGGCA CCATCAAAAC 5700

CTGGGACGAC CCGCAGATCG CTGCGCTCAA CCCCGGCGTG AACCTGCCCG GCACCGCGGT 5760

AGTTCCGCTG CACCGCTCCG ACGGGTCCGG TGACACCTTC TTGTTCACCC AGTACCTGTC 5820

CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC GCCCGGCTTC GGCACCACCG TCGACTTCCC 5880

GCCGGTGCCG GGTGCGCTGG GTGAGAACGG CAACGGCGGC ATGGTGACCG GTTGCGCCGA 5940

GACACCGGGC TGCGTGGCCT ATATCGGCAT CAGCTTCCTC GACCAGGCCA GTCAACGGGG 6000

ACTCGGCGAG GCCCAACTAG GCAATAGCTC TGGCAATTTC TTGTTGCCCG ACGCGCAAAG 6060

CATTCAGGCC GCGGCGGCTG GCTTCGCATC GAAAACCCCG GCGAACCAGG CGATTTCGAT 6120

GATCGACGGG CCCGCCCCGG ACGGCTACCC GATCATCAAC TACGAGTACG CCATCGTCAA 6180

CAACCGGCAA AAGGACGCCG CCACCGCGCA GACCTTGCAG GCATTTCTGC ACTGGGCGAT 6240

CACCGACGGC AACAAGGCCT CGTTCCTCGA CCAGGTTCAT TTCCAGCCGC TGCCGCCGGC 6300

GGTGGTGAAG TTGTCTGACG CGTTGATCGC GACGATTTCC AGCGCTGAGA TGAAGACCGA 6360

TGCCGCTACC CTCGCGCAGG AGGCAGGTAA TTTCGAGCGG ATCTCCGGCC ACCTGAAAAC 6420

CCAGATCGAC CAGGTGGAGT CGACGGCAGG TTCGTTGCAG GGCCAGTGGC GCGGCGCGGC 6480

GGGGACGGCC GCCCAGGCCG CGGTGGTGCG CTTCCAAGAA GCAGCCAATA AGCAGAAGCA 6540

GGAACTCGAC GAGATCTCGA CGAATATTCG TCAGGCCGGC GTCCAATACT CGAGGGCCGA 6600

CGAGGAGCAG CAGCAGGCGC TGTCCTCGCA AATGGGCTTT GTGCCCACAA CQGCCGCCTC 6660

GCCGCCGTCG ACCGCTGCAG CGCCACCGGC ACCGGCGACA CCTGTTGCCC CCCCACCACC 6720

GGCCGCCGCC AACACGCCGA ATGCCCAGCC GGGCGATCCC AACGCAGCAC CTCGGCCGGC 6780

CGACCCGAAC GCACCGCCGC CACCTGTCAT TGCCCCAAAC GCACCCCAAC CTGTCCGGAT 6840

CGACAACCCG GTTGGAGGAT TCAGCTTCGC GCTGCCTGCT GGCTGGGTGG AGTCTGACGC 6900

CGCCCACTTC GACTACGGTT CAGCACTCCT CAGCAAAACC ACCGGGGACC CGCCATTTCC 6960

CGGACAGCCG CCGCCGGTGG CCAATGACAC CCGTATCGTG CTCGGCCGGC TAGACCAAAA 7020

Fig. 5E

GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGCCGCG GCCCGGTTGG GCTCGGACAT 7080

GGGTGAGTTC TATATGCCCT ACCCGGGCAC CCGGATCAAC CAGGAAACCG TCTCGCTTGA 7140

CGCCAACGGG GTGTCTGGAA GCGCGTCGTA TTACGAAGTC AAGTTCAGCG ATCCGAGTAA 7200

GCCGAACGGC CAGATCTGGA CGGGCGTAAT CGGCTCGCCC GCGGCGAACG CACCGGACGC 7260

CGGGCCCCCT CAGCGCTGGT TTGTGGTATG GCTCGGGACC GCCAACAACC CGGTGGACAA 7320

GGGCGCGGCC AAGGCGCTGG CCGAATCGAT CCGGCCTTTG GTCGCCCCGC CGCCGGCGCC 7380

GGCACCGGCT CCTGCAGAGC CGGCTCCGGC GCCGGCGCCG GCCGGGGAAG TCGCTCCTAC 7440

CCCGACGACA CCGACACCGC AGCGGACCTT ACCGGCCTGA GAATTCTGCA GATATCCATC 7500

ACACTGGCGG CCGCTCGAGC ACCACCACCA CCACCACTGA GATCCGGCTG CTAACAAAGC 7560

CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCCTTGG 7620

GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGAACTATAT CCGGAT 7676

Fig. 5F

```
Met Gly His His His His His His Val Ile Asp Ile Ile Gly Thr Ser
1               5                  10                  15

Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
            20                  25                  30

Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
        35                  40                  45

Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
    50                  55                  60

Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
65                  70                  75                  80

Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
                85                  90                  95

Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
            100                 105                 110

Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
        115                 120                 125

Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
    130                 135                 140

Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
145                 150                 155                 160

Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
                165                 170                 175

Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
            180                 185                 190

Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
        195                 200                 205

Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
    210                 215                 220
```

Fig. 5B

```
Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
225                 230                 235                 240

Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
                245                 250                 255

Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
            260                 265                 270

Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
        275                 280                 285

Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp
    290                 295                 300

Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser
305                 310                 315                 320

Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
                325                 330                 335

Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
            340                 345                 350

Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
        355                 360                 365

Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
    370                 375                 380

Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
385                 390                 395                 400

Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
                405                 410                 415

Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
            420                 425                 430

Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
        435                 440                 445

Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
    450                 455                 460

Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
465                 470                 475                 480
```

Fig 5 H

```
Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
                485                 490                 495

Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
            500                 505                 510

Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
        515                 520                 525

Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
    530                 535                 540

Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
545                 550                 555                 560

Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
                565                 570                 575

Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
            580                 585                 590

Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
        595                 600                 605

Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
    610                 615                 620

Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
625                 630                 635                 640

Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
                645                 650                 655

Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
            660                 665                 670

Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
        675                 680                 685

Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
    690                 695                 700

Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
705                 710                 715                 720

Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
                725                 730                 735
```

Fig 5 I

```
Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
            740                 745                 750

Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
        755                 760                 765

Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
    770                 775                 780

Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
785                 790                 795                 800

Pro Ala
```

Fig. 5J

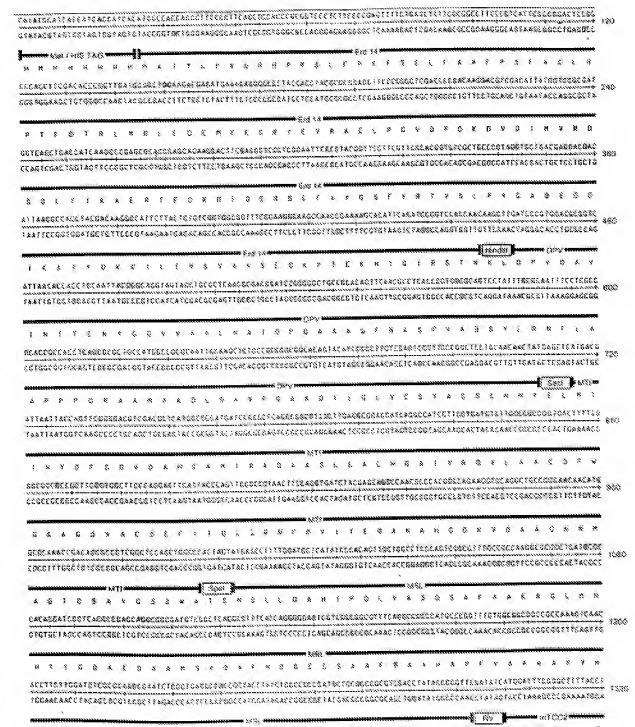


Fig 6A

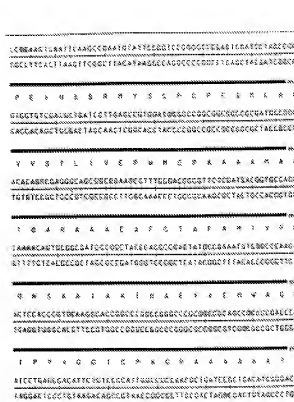


Fig 6B

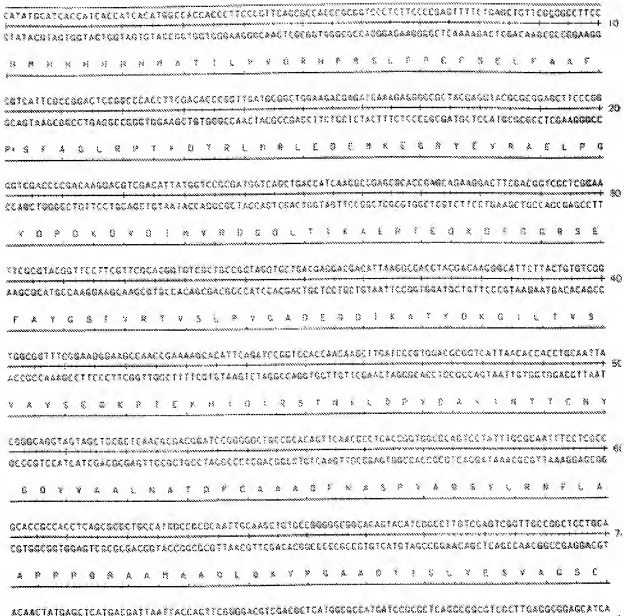


Fig 7A

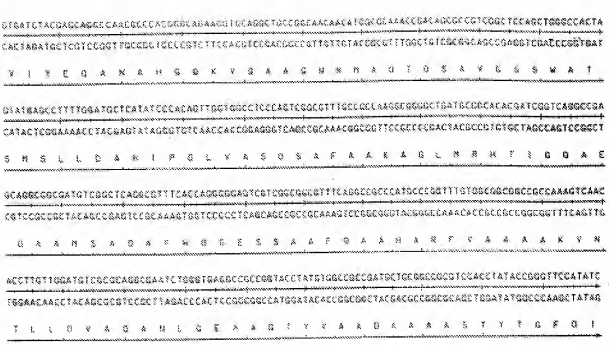


Fig. 7B

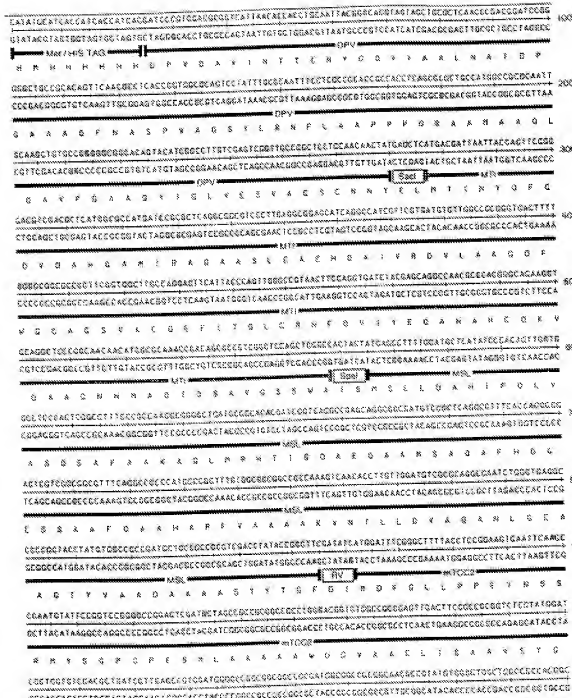

Met/His TAG
DPV
DPV
DPV
SacI
MTI
MTI
SpeI
MTI
MSL
MSL
MSL
AV
mTOCE
mTOCE

Fig 8A

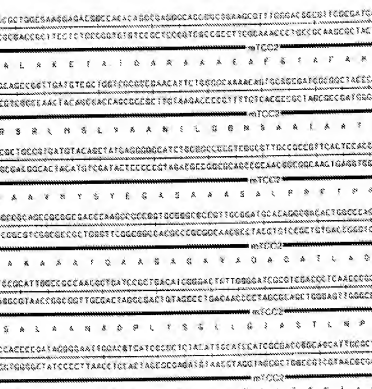

mTOC2
mTOC2
mTOC2
mTOC2
mTOC2
mTOC2
mTOC2
mTOC2
mTOC2
mTOC2
mTOC3
pET poslinker
XhoI
mTOC3

Fig. 83

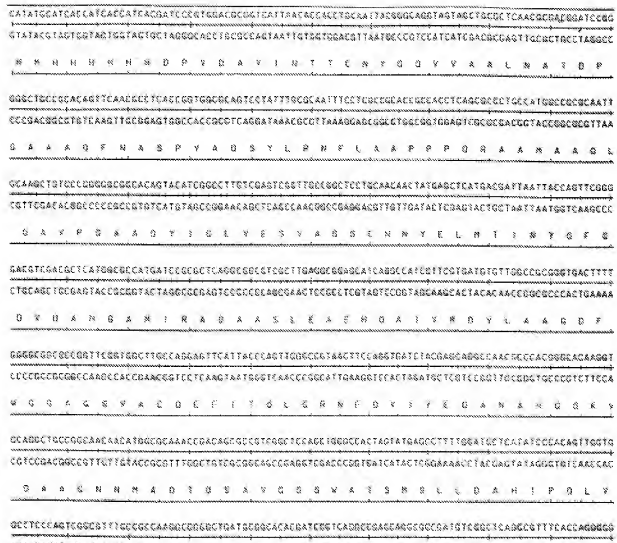


Fig. 9A

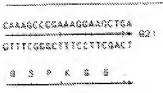


Fig. 9B

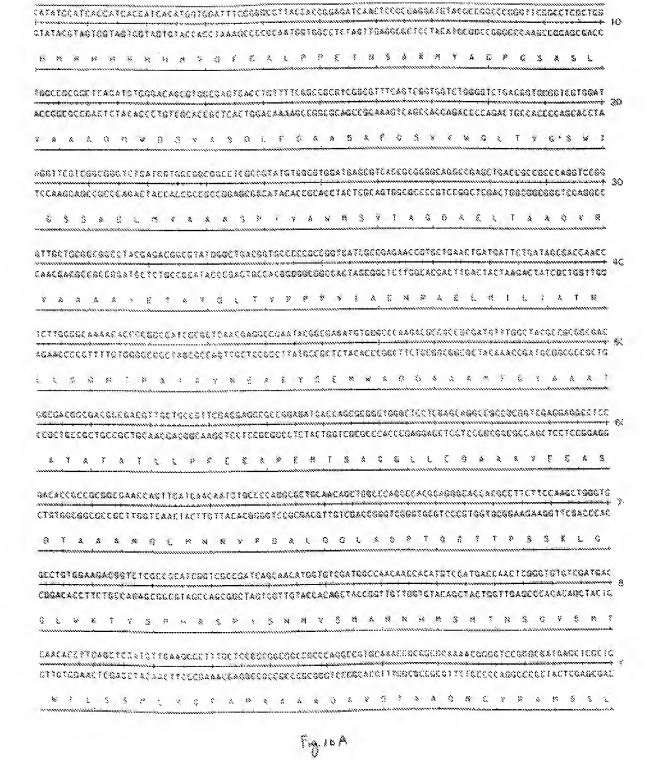


Fig 10A

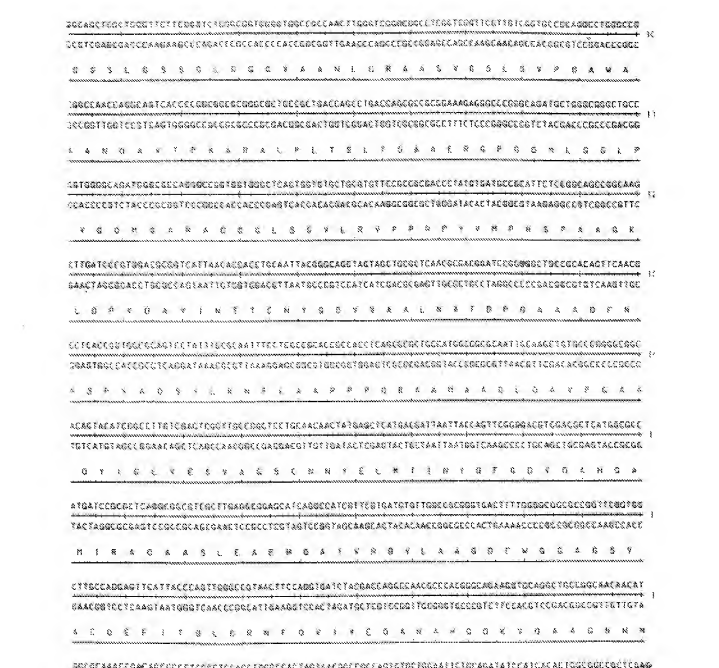


Fig. 1B

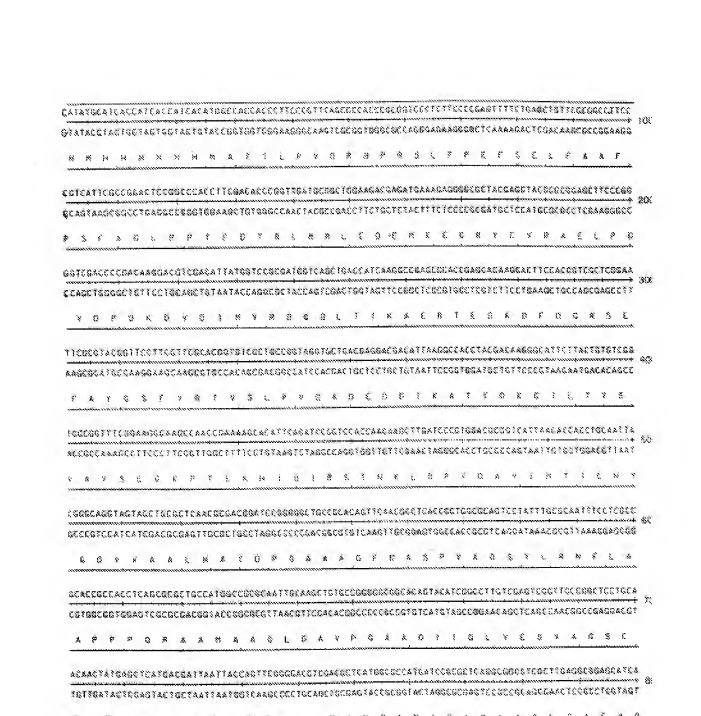
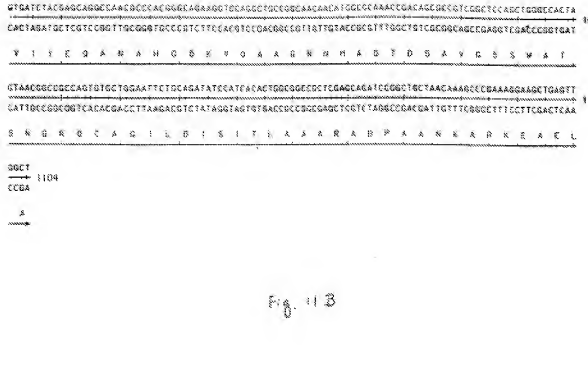


Fig 11A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V I Y E Q A N A H G Q K V Q A A G N N M A D T D S A V G S S W A T
GTAACGGCCGCCAGTGTGCTGGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCGAGCAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTT
CATTGCCGGCGGTCACACGACCTTAAGACGTCTATAGGTAGTGTGACCGCCGGCGAGCTCGTCTAGGCCGACGATTGTTTCGGGCTTTCCTTCGACTCAA
S N G R G C A G I L E I S I T L A A A R A D P A A N K A R K E A E L
GGCT
1104
CCGA
A

Fig. 13

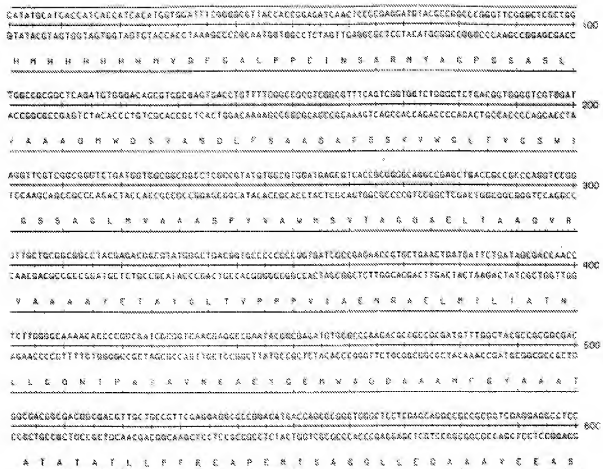


Fig 12 A

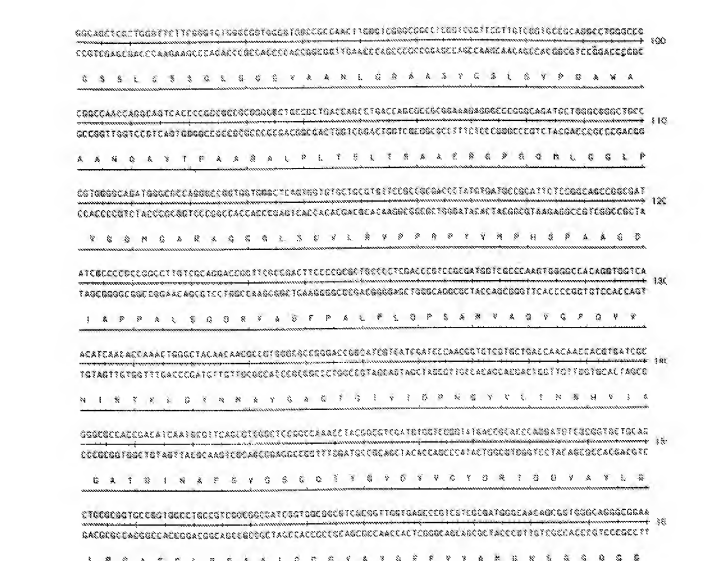


Fig. 23

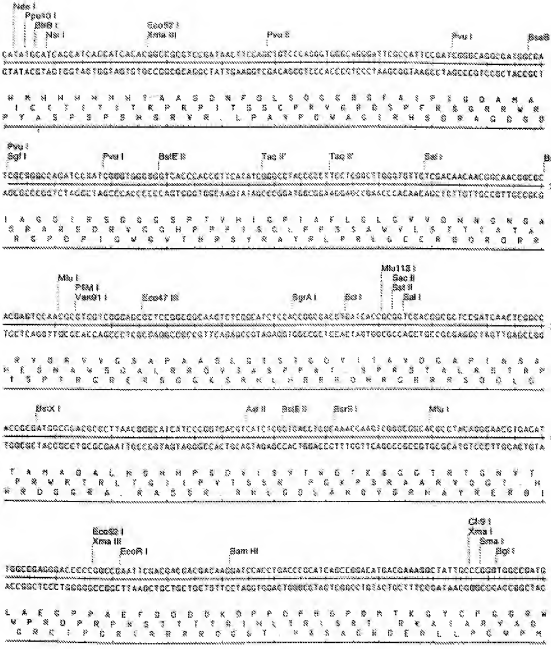

Nde I
PpuMI
BbsI
Nsi I
EcoS2 I
Xma III
Pvu II
Pvu I
BssS I
100
Pvu I
Sgf I
Pvu I
BstE II
Taq II
Taq II
Sal I
BssS I
200
Mlu I
PflM I
Van91 I
Ecc47 III
SgrA I
Bcl I
Mlu11 I
Sac II
Sst II
Sal I
300
BstX I
Age II
BstEII
BsrG I
Mlu I
400
EcoS2 I
Xma III
EcoR I
Bam HI
Cla I
Xma I
Sma I
Bgl I
500

Fig. 13A

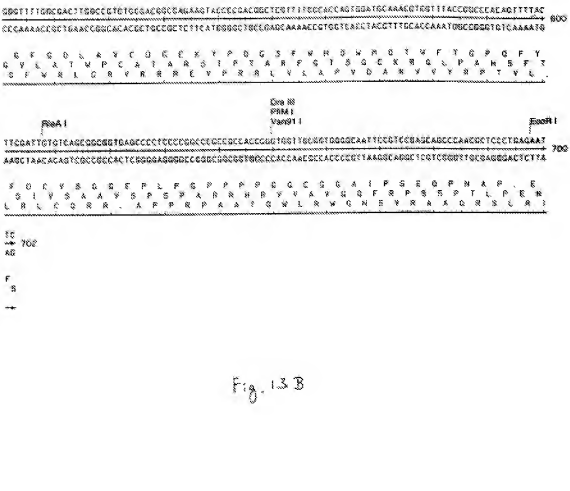


Fig. 13B

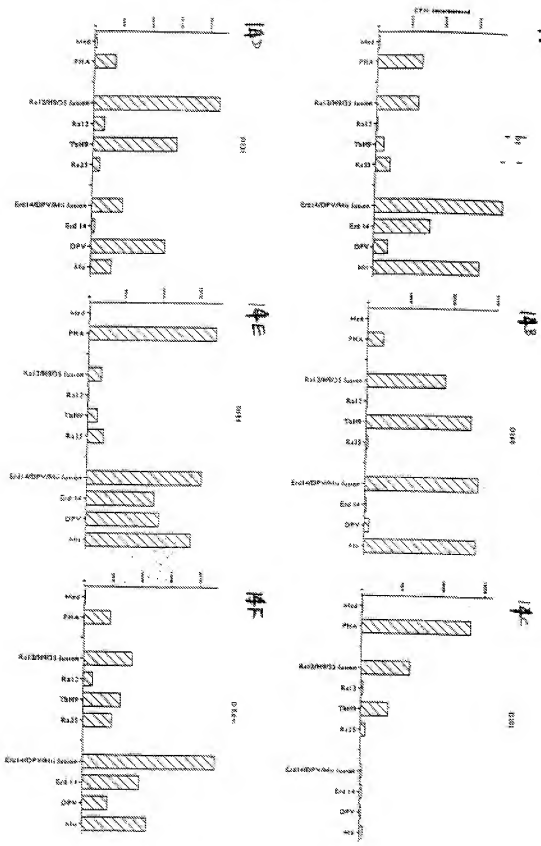

T Cell Proliferation Ex Assay 033098
14A
14B
14C
14D
14E
14F
Med
PHA
Ra13/9RD3 fusion
Ra12
Tbh9
Ra23
Ra13/9RD3 fusion
Ra12
Tbh9
Ra23
Ent14/DPV/Ra fusion
Ent 14
DPV
Alb

Fig. 14A-14F

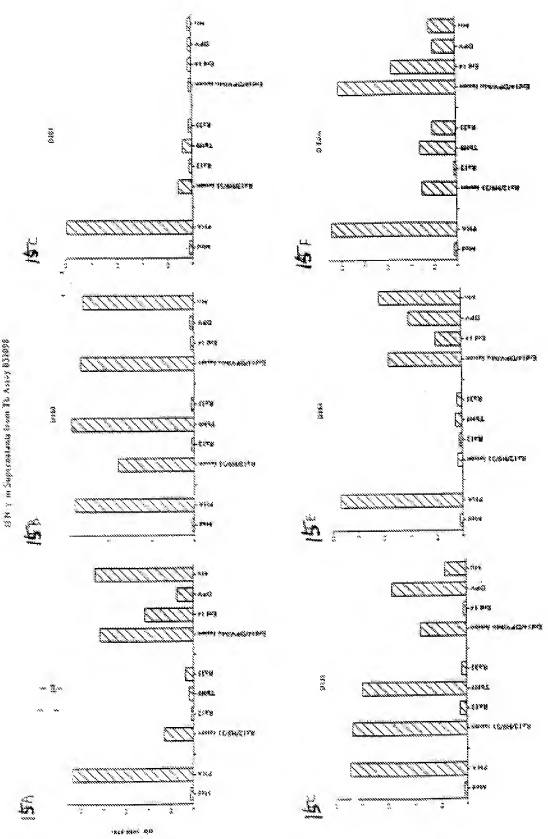


Fig. 15A-15F

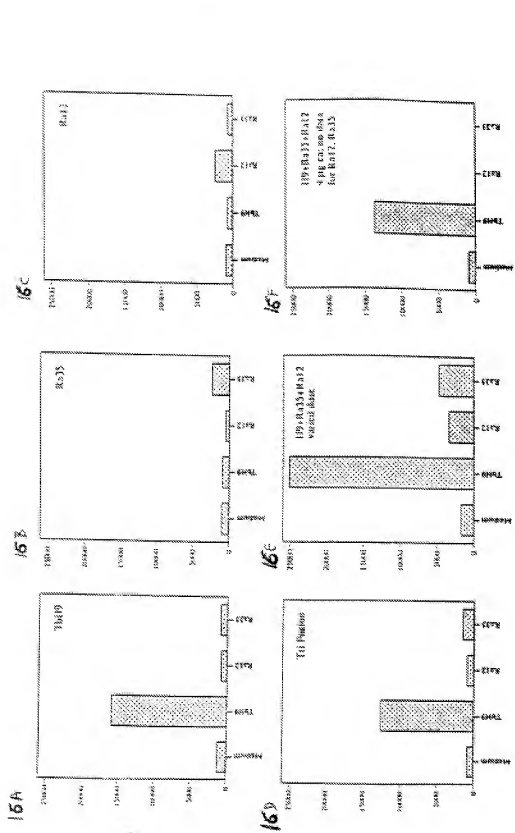

Antigens Formulated in SBAS16
16A
Tb419
16B
Ra35
16C
Ra12
16D
Tri Fusion
16E
139-Ra35-Ra12
without Alum
16F
139-Ra35-Ra12
4 µg CpG 1826
for Ra12-Ra35

Fig 16A-16F

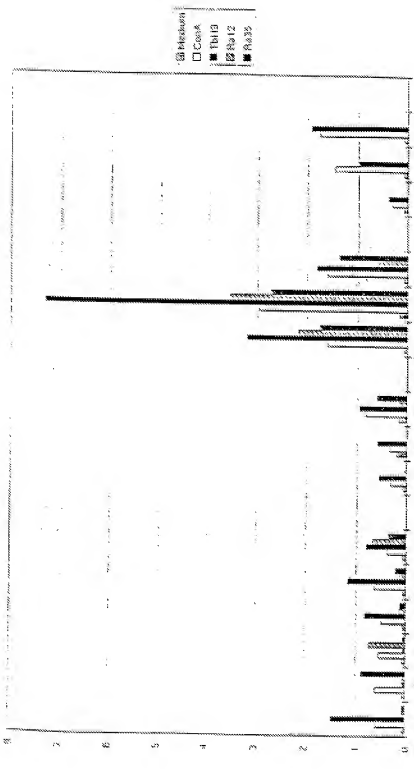

IFN Production (ng/ml)
Medium
Con A
Rb19
Rb12
Rb35
saline
TBH9 DNA (3m, C
TBH9 DNA (3m, B
TBH9 DNA (3m, A
pH6.7 + Al(OH)3 (4ug)
H9+Rb35+Rb12 in Al(OH)3
Fusion in Al(OH)3
H9+Rb35+Rb12 in SBA52
SBA52
Fusion in SBA52
H9+Rb35+Rb12 in SBA516
SBA516
Fusion in SBA516
Rb12 in SBA516
Rb35 in SBA516
H9 in SBA516

Fig. 17

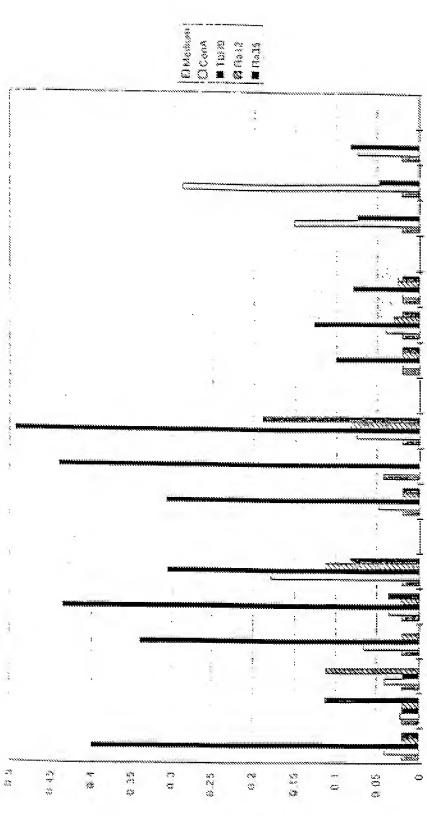

IL-6 Production (ng/ml)
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Medium
ConA
1b/39
Ra12
Ra35
H9 in SBAS1c
Ra35 in SBAS1c
Ra12 in SBAS1c
Fusion in SBAS1c
H9+Ra35+Ra12 in SBAS1c
SBAS1c
H9+Ra35+Ra12 in SBAS1c (4ug)
SBAS1c (4ug)
Fusion in SBAS2
H9+Ra35+Ra12 in SBAS2
SBAS2
H9+Ra35+Ra12 in SBAS2 (4ug)
SBAS2 (4ug)
Fusion in Al(OH)3
H9+Ra35+Ra12 in Al(OH)3
Al(OH)3
H9+Ra35+Ra12 in Al(OH)3 (4ug)
Al(OH)3 (4ug)
TsH9 DNA i.m. A
TsH9 DNA i.m. B
TsH9 DNA i.m. C
saline

Fig 18

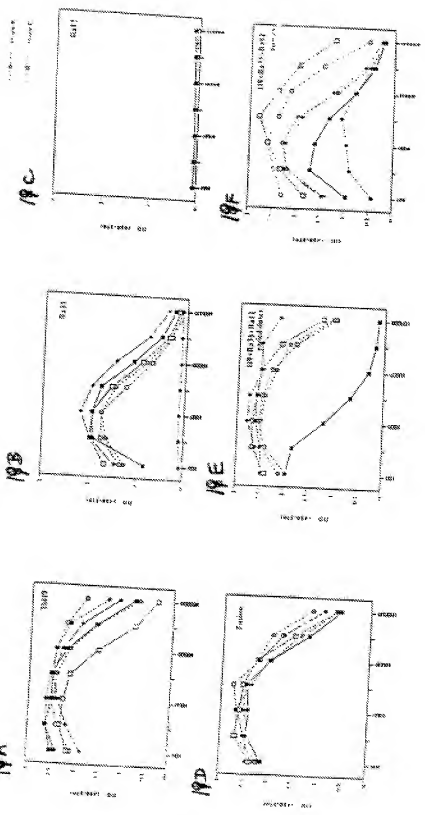
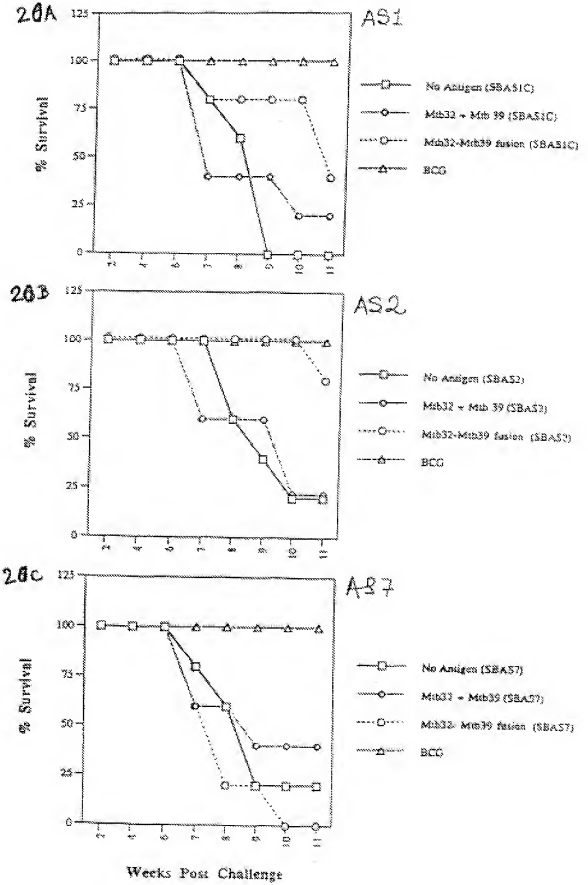
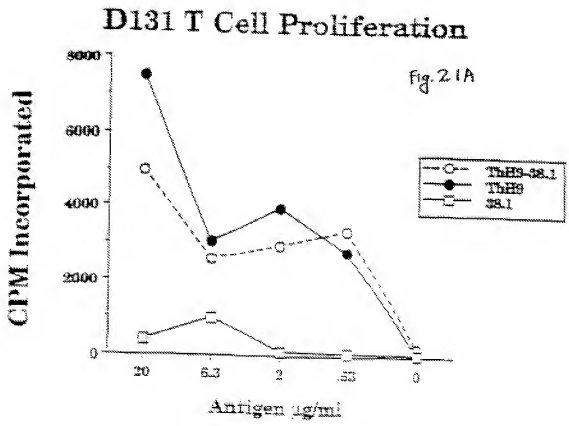

Serum Antibody to TMP
Antigen Immobilized in SPASA
19A
19B
19C
19D
19E
19F

Fig 19A - 19F

Fig. 20A - 20C


20A
AS1
% Survival
No Antigen (SBAS1C)
Mtb32 + Mtb 39 (SBAS1C)
Mtb32-Mtb39 fusion (SBAS1C)
BCG
20B
AS2
% Survival
No Antigen (SBAS2)
Mtb32 + Mtb 39 (SBAS2)
Mtb32-Mtb39 fusion (SBAS2)
BCG
20C
AS7
% Survival
No Antigen (SBAS7)
Mtb32 + Mtb39 (SBAS7)
Mtb32- Mtb39 fusion (SBAS7)
BCG
Weeks Post Challenge


D131 T Cell Proliferation
Fig. 21A
CPM Incorporated
8000
6000
4000
2000
0
20
6.3
2
.63
0
Antigen µg/ml
ThH9-38.1
ThH9
38.1

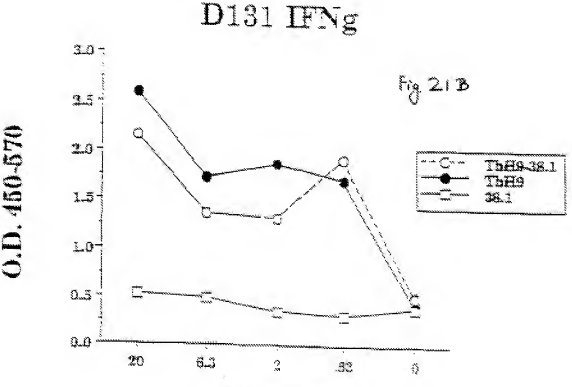

D131 IFNg
Fig. 21B
O.D. 450-570
3.0
2.5
2.0
1.5
1.0
0.5
0.0
20
6.3
2
.63
0
Antigen µg/ml
ThH9-38.1
ThH9
38.1

Fig. 21A + 21B

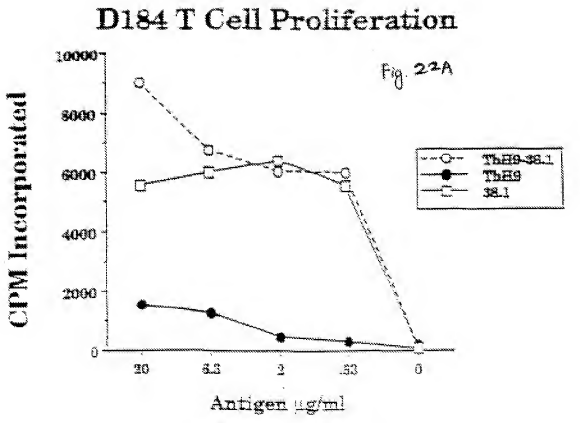
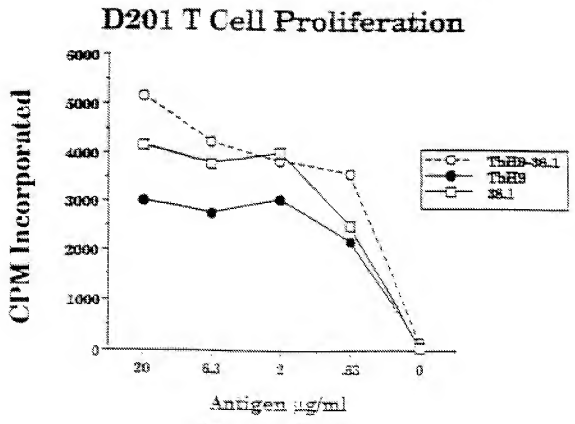

D184 T Cell Proliferation
Fig 22A
CPM Incorporated
10000
8000
6000
4000
2000
0
20
6.3
2
.63
0
Antigen µg/ml
ThH9-38.1
ThH9
38.1
D184 IFNg
Fig 22B
O.D. 450-570
3.0
2.5
2.0
1.5
1.0
0.5
0.0
20
6.3
2
.63
0
Antigen µg/ml
ThH9-38.1
ThH9
38.1

Fig. 22A + 22B

Fig. 23A



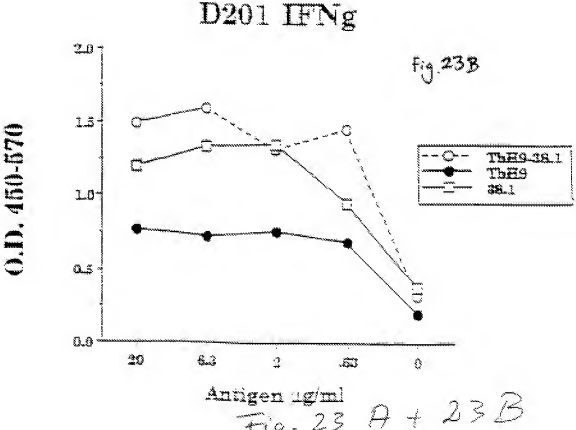


Fig. 23B

Fig. 23 A + 23 B